

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claim 1 (previously presented): A method for improving plant growth characteristics selected from one or more of increased yield, increased growth rate and modified architecture, said method comprising:

(a) introducing into a plant a gene construct comprising a nucleic acid molecule encoding a B-type CDK protein operably linked to a promoter, said CDK protein comprising a PPTALRE motif (SEQ ID NO:26) with no mismatches or with a mismatch at position 2 and/or 4 from left to right, a catalytic kinase domain, and a T-loop activation kinase domain, to obtain T0 transformants;

(b) growing the T0 transformants to obtain T1 seed;

(c) germinating the T1 seed to obtain T1 plants;

(d) selecting T1 plants or progeny thereof comprising the nucleic acid molecule encoding the B-type CDK protein;

(e) measuring in a T1 selected plant or progeny thereof of step (d), a parameter selected from the group consisting of: aboveground plant area; plant height; panicle number, total seed number; number of filled seeds; total weight of seeds; harvest index; or thousand kernel weight;

(f) correlating an increase in a parameter of step (e) in a T1 plant or progeny thereof compared to a control wild type plant, with a plant having increased yield, increased growth rate or modified architecture.

Claim 2 (canceled)

Claim 3 (currently amended): **[[A]] The Method according to claim 1, wherein said B-type CDK is derived from a plant-source.**

Claim 4 (currently amended): **[[A]] The method according to claim 3, wherein said B-type CDK derived from a plant is preferably from a dicotyledonous plant, further preferably from the family *Brassicaceae*, more preferably from *Arabidopsis thaliana*.**

Claim 5 (currently amended): **[[A]] The method according to claim 3, wherein said B-type CDK is a class 1 B-type CDK, preferably a CDK B1;1 from *Arabidopsis thaliana* or a CDK B1;2 from *Arabidopsis thaliana*.**

Claim 6 (currently amended): **[[A]] The method according to claim 3, wherein said B-type CDK is a class 2 B-type CDK, preferably a CDK B2;2 from *Arabidopsis thaliana*.**

Claim 7 (currently amended): **[[A]] The method according to claim 5, wherein said CDK B1;1 nucleic acid is as represented by SEQ ID NO: 1 or by a portion thereof, or by a nucleic acid sequence capable of hybridising therewith, and wherein the CDK B1;1 protein is as represented by has the amino acid sequence of SEQ ID NO: 2.**

Claim 8 (currently amended): **[[A]] The method according to claim 5, wherein the CDK B1;2 protein has the amino acid sequence of SEQ ID NO: 4.**

Claim 9 (currently amended): **[[A]] The method according to claim 6, wherein the CDK B2;2 protein has the amino acid sequence of SEQ ID NO: 6.**

Claim 10 (canceled)

Claim 11 (currently amended): The ~~[[M]]~~ method according to claim 5, wherein expression of said CDK B1;1 nucleic acid is driven by a promoter active in young, expanding tissue.

Claim 12 (currently amended): The ~~[[M]]~~ method according to claim 5 or 6, wherein expression of said CDK B1;2 nucleic acid and wherein expression of said CDK B2;2 nucleic acid is driven by a constitutive promoter~~[[,]] preferably wherein said promoter is a GOS 2 promoter.~~

Claim 13 (currently amended): The ~~[[M]]~~ method according to claim 1, wherein said increased yield comprises one or more of: an increase in area, an increase in the number of panicles, an increase in height, an increase in the number of seeds, an increase in the number of filled seeds, an increase in the total weight of seeds, an increase in thousand kernel weight (TKW) and an increase in harvest index, each relative to control plants.

Claim 14 (currently amended): The ~~[[M]]~~ method according to claim 1, wherein said modified architecture includes one or more of: increase in aboveground area, increase in the number of panicles and an increase in height.

Claim 15 (canceled)

Claims 16 - 19 (cancelled)

Claim 20 (currently amended): A ~~[[M]]~~ method for the production of a transgenic plant having improved growth characteristics selected from any one or more of: increased yield, increased

growth rate and modified architecture, which growth characteristics are improved relative to growth characteristics of corresponding wild type plants, said method comprising the steps of:

- (a) introducing into a plant or a plant cell a gene construct comprising a nucleic acid molecule encoding a B-type CDK protein, operably linked to a promoter, said B-type CDK comprising a PPTALRE motif (SEQ ID NO:26) with no mismatches or with a mismatch at position 2 and/or 4 from left to right, a catalytic kinase domain, and a T-loop activation kinase domain; or
- (b) a nucleic acid encoding a CDK mutant, which CDK mutant comprises SEQ ID NO:9 having at least one of a Y substituted for an H at position 4, V substituted for a D at position 79 or an A substituted for a T at position 152; SEQ ID NO:10 having an I substituted for a T at position 30; or SEQ ID NO:11 having at least one of an E substituted for a V at position 5, an R substituted for an S at position 122, or a K substituted for an E at position 143;
- (c) cultivating the plant cell under conditions promoting regeneration and mature plant growth; and
- (d) selecting a plant having increased yield, increased growth rate, or modified architecture.

Claims 21-31 (canceled)

Claim 32 (previously presented): The method of claim 7 wherein the CDK B1:1 protein having the amino acid sequence of SEQ ID NO:2 is encoded by a nucleic acid molecule having the sequence of SEQ ID NO:1.

Claim 33 (previously presented): The method of claim 8 wherein the CDK B1:2 protein having the amino acid sequence of SEQ ID NO:4 is encoded by the nucleic acid molecule having the sequence of SEQ ID NO:3.

Claim 34 (previously presented): The method of claim 9 wherein the CDK B2;2 protein having the amino acid sequence of SEQ ID NO:6 is encoded by a nucleic acid molecule having the sequence of SEQ ID NO:5.

Claim 35 (previously presented): The method of claim 11 wherein the promoter active in young, expanding tissue is a beta expansin promoter having the nucleotide sequence of SEQ ID NO:14.

Claim 36 (previously presented): The method of claim 12 wherein the constitutive promoter is a GOS2 promoter having the nucleotide sequence of SEQ ID NO:15.